ALIGNMENT 1: SEQ ID NO:7

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                          1                    30 31                    60 61                    90 91                    120
Original_Seq7     GAATTCACGATGGCCAACAAATACAATTCC GAAATCCTGAACAATATCATCCTGAACCTG CGTTACAAAGACAACAATCTGATCGATCTG TCTGGTTACGGTGCTAAAGTTGAAGTATAC
Substitute_Seq7   GAATTCACGATGGCCAACAAATACAATTCC GAAATCCTGAACAATATCATCCTGAACCTG CGTTACAAAGACAACAATCTGATCGATCTG TCTGGTTACGGTGCTAAAGTTGAAGTATAC
Amended_Seq7      GAATTCACGATGGCCAACAAATACAATTCC GAAATCCTGAACAATATCATCCTGAACCTG CGTTACAAAGACAACAATCTGATCGATCTG TCTGGTTACGGTGCTAAAGTTGAAGTATAC
Original_Fig4     GAATTCACGATGGCCAACAAATACAATTCC GAAATCCTGAACAATATCATCCTGAACCTG CGTTACAAAGACAACAATCTGATCGATCTG TCTGGTTACGGTGCTAAAGTTGAAGTATAC


                          121                  150 151                  180 181                  210 211                  240
Original_Seq7     GACGGTGTTGAACTGAATGACAAGAACCAG TTCAAACTGACCTCTTCCGCTAACTCTAAG ATCCGTGTTACTCAGAATCAGAACATCATC TTCAACTCCGTATTCCTGGACTTCTCTGTT
Substitute_Seq7   GACGGTGTTGAACTGAATGACAAGAACCAG TTCAAACTGACCTCTTCCGCTAACTCTAAG ATCCGTGTTACTCAGAATCAGAACATCATC TTCAACTCCGTATTCCTGGACTTCTCTGTT
Amended_Seq7      GACGGTGTTGAACTGAATGACAAGAACCAG TTCAAACTGACCTCTTCCGCTAACTCTAAG ATCCGTGTTACTCAGAATCAGAACATCATC TTCAACTCCGTATTCCTGGACTTCTCTGTT
Original_Fig4     GACGGTGTTGAACTGAATGACAAGAACCAG TTCAAACTGACCTCTTCCGCTAACTCTAAG ATCCGTGTTACTCAGAATCAGAACATCATC TTCAACTCCGTATTCCTGGACTTCTCTGTT


                          241                  270 271                  300 301                  330 331                  360
Original_Seq7     TCCTTCTGGATTCGTATCCCGAAATACAAG AACGACGGTATCCAGAATTACATCCACAAT GAATACACCATCATCAACTGCATGAAGAAT AACTCTGGTTGGAAGATCTCCATCCGCGGT
Substitute_Seq7   TCCTTCTGGATCGTATCCCGAAATACAAG AACGACGGTATCCAGAATTACATCCACAAT GAATACACCATCATCAACTGCATGAAGAAT AACTCTGGTTGGAAGATCTCCATCCGCGGT
Amended_Seq7      TCCTTCTGGATTCGTATCCCGAAATACAAG TTCAAACTGACCTCTTCCGCTAACTCTAAG GAATACACCATCATCAACTGCATGAAGAAT AACTCTGGTTGGAAGATCTCCATCCGCGGT
Original_Fig4     TCCTTCTGGATTCGTATCCCGAAATACAAG AACGACGGTATCCAGAATTACATCCACAAT GAATACACCATCATCAACTGCATGAAGAAT AACTCTGGTTGGAAGATCTCCATCCGCGGT


                          361                  390 391                  420 421                  450 451                  480
Original_Seq7     AACCGTATCATCTGGACTCTGATCGATATC AACGGTAAGACCCAAATCTGTATTCTTCGAA TACAACATCCGTGAAGACATCTCTGAATAC ATCAATCGCTGGTTCTTCGTTACCATCACC
Substitute_Seq7   AACCGTATCATCTGGACTCTGATCGATATC AACGGTAAGACCCAAATCTGTATTCTTCGAA TACAACATCCGTGAAGACATCTCTGAATAC ATCAATCGCTGGTTCTTCGTTACCATCACC
Amended_Seq7      AACCGTATCATCTGGACTCTGATCGATATC AACGGTAAGACCCAAATCTGTATTCTTCGAA TACAACATCCGTGAAGACATCTCTGAATAC ATCAATCGCTGGTTCTTCGTTACCATCACC
Original_Fig4     AACCGTATCATCTGGACTCTGATCGATATC AACGGTAAGACCCAAATCTGTATTCTTCGAA TACAACATCCGTGAAGACATCTCTGAATAC ATCAATCGCTGGTTCTTCGTTACCATCACC


                          481                  510 511                  540 541                  570 571                  600
Original_Seq7     AATAACCTGAACAATGCTAAAATCTACATC AACGGTAAACTGGAATCTAATACCGACATC AAAGACATCCGTGAAGTTATCGCTAACGGT GAAATCATCTTCAAACTGGACGGTGACATC
Substitute_Seq7   AATAACCTGAACAATGCTAAAATCTACATC AACGGTAAACTGGAATCTAATACCGACATC AAAGACATCCGTGAAGTTATCGCTAACGGT GAAATCATCTTCAAACTGGACGGTGACATC
Amended_Seq7      AATAACCTGAACAATGCTAAAATCTACATC AACGGTAAACTGGAATCTAATACCGACATC AAAGACATCCGTGAAGTTATCGCTAACGGT GAAATCATCTTCAAACTGGACGGTGACATC
Original_Fig4     AATAACCTGAACAATGCTAAAATCTACATC AACGGTAAACTGGAATCTAATACCGACATC AAAGACATCCGTGAAGTTATCGCTAACGGT GAAATCATCTTCAAACTGGACGGTGACATC


                          601                  630 631                  660 661                  690 691                  720
Original_Seq7     GATCGTACCCAGTTCATCTGGATGAAATAC TTCTCCATCTTCAACACCGAACTGTCTCAG TCCAATATCGAAGAACGGTACAAGATCCAG TCTTACTCCGAATACCTGAAAGACTTCTGG
Substitute_Seq7   GATCGTACCCAGTTCATCTGGATGAAATAC TTCTCCATCTTCAACACCGAACTGTCTCAG TCCAATATCGAAGAACGGTACAAGATCCAG TCTTACTCCGAATACCTGAAAGACTTCTGG
Amended_Seq7      GATCGTACCCAGTTCATCTGGATGAAATAC TTCTCCATCTTCAACACCGAACTGTCTCAG TCCAATATCGAAGAACGGTACAAGATCCAG TCTTACTCCGAATACCTGAAAGACTTCTGG
Original_Fig4     GATCGTACCCAGTTCATCTGGATGAAATAC TTCTCCATCTTCAACACCGAACTGTCTCAG TCCAATATCGAAGAACGGTACAAGATCCAG TCTTACTCCGAATACCTGAAAGACTTCTGG


                          721                  750 751                  780 781                  810 811                  840
Original_Seq7     GGTAATCCGCTGATGTACAACAAAGAATAC TATATGTTCAATGCTGGTAACAAGAACTCT TACATCAAACTGAAGAAAGACTCTCCGGTT GGTGAAATCCTGACTCGTTCCAAATACAAC
Substitute_Seq7   GGTAATCCGCTGATGTACAACAAAGAATAC TATATGTTCAATGCTGGTAACAAGAACTCT TACATCAAACTGAAGAAAGACTCTCCGGTT GGTGAAATCCTGACTCGTTCCAAATACAAC
Amended_Seq7      GGTAATCCGCTGATGTACAACAAAGAATAC TATATGTTCAATGCTGGTAACAAGAACTCT TACATCAAACTGAAGAAAGACTCTCCGGTT GGTGAAATCCTGACTCGTTCCAAATACAAC
Original_Fig4     GGTAATCCGCTGATGTACAACAAAGAATAC TATATGTTCAATGCTGGTAACAAGAACTCT TACATCAAACTGAAGAAAGACTCTCCGGTT GGTGAAATCCTGACTCGTTCCAAATACAAC


                          841                  870 871                  900 901                  930 931                  960
Original_Seq7     CAGAACTCTAAATACATCAACTACCGCGAC CTGTACATCGGTGAAAAGTTCATCATCCGT CGCAAATCTAACTCTCAGTCCATCAATGAT GACATCGTACGTAAAGAAGACTACATCTAC
Substitute_Seq7   CAGAACTCTAAATACATCAACTACCGCGAC CTGTACATCGGTGAAAAGTTCATCATCCGT CGCAAATCTAACTCTCAGTCCATCAATGAT GACATCGTACGTAAAGAAGACTACATCTAC
Amended_Seq7      CAGAACTCTAAATACATCAACTACCGCGAC CTGTACATCGGTGAAAAGTTCATCATCCGT CGCAAATCTAACTCTCAGTCCATCAATGAT GACATCGTACGTAAAGAAGACTACATCTAC
Original_Fig4     CAGAACTCTAAATACATCAACTACCGCGAC CTGTACATCGGTGAAAAGTTCATCATCCGT CGCAAATCTAACTCTCAGTCCATCAATGAT GACATCGTACGTAAAGAAGACTACATCTAC


                          961                  990 991                  1020 1021                 1050 1051                 1080
Original_Seq7     CTGGACTTCTTCAACCTGAATCAGGAATGG CGTGTATACACCTACAAGTACTTCAAGAAA GAAGAAGAAAAGCTTTTCCTGGCTCCGATC TCTGATTCCGACGAACTCTACAACACCATC
Substitute_Seq7   CTGGACTTCTTCAACCTGAATCAGGAATGG CGTGTATACACCTACAAGTACTTCAAGAAA GAAGAAGAAAAGCTTTTCCTGGCTCCGATC TCTGATTCCGACGAACTCTACAACACCATC
Amended_Seq7      CTGGACTTCTTCAACCTGAATCAGGAATGG CGTGTATACACCTACAAGTACTTCAAGAAA GAAGAAGAAAAGCTTTTCCTGGCTCCGATC TCTGATTCCGACGAACTCTACAACACCATC
Original_Fig4     CTGGACTTCTTCAACCTGAATCAGGAATGG CGTGTATACACCTACAAGTACTTCAAGAAA GAAGAAGAAAAGCTTTTCCTGGCTCCGATC TCTGATTCCGACGAACTCTACAACACCATC


                          1081                 1110 1111                 1140 1141                 1170 1171                 1200
Original_Seq7     CAGATCAAAGAATACGACGAACAGCCGACC TACTCTTGCCAGCTGCTGTTCAAGAAAGAT GAAGAATCTACTGACGAAATCGGTCTGATC GGTATCCACCGTTTCTACGAATCTGGTATC
Substitute_Seq7   CAGATCAAAGAATACGACGAACAGCCGACC TACTCTTGCCAGCTGCTGTTCAAGAAAGAT GAAGAATCTACTGACGAAATCGGTCTGATC GGTATCCACCGTTTCTACGAATCTGGTATC
Amended_Seq7      CAGATCAAAGAATACGACGAACAGCCGACC TACTCTTGCCAGCTGCTGTTCAAGAAAGAT GAAGAATCTACTGACGAAATCGGTCTGATC GGTATCCACCGTTTCTACGAATCTGGTATC
Original_Fig4     CAGATCAAAGAATACGACGAACAGCCGACC TACTCTTGCCAGCTGCTGTTCAAGAAAGAT GAAGAATCTACTGACGAAATCGGTCTGATC GGTATCCACCGTTTCTACGAATCTGGTATC


                          1201                 1230 1231                 1260 1261                 1290 1291                 1320
Original_Seq7     GTATTCGAAGAATACAAAGACTACTTCTGC ATCTCCAAATGGTACCTGAAGGAAGTTAAA CGCAAACCGTACAACCTGAAACTGGGTTGC AATTGGCAGTTCATCCCGAAAGACGAAGGT
Substitute_Seq7   GTATTCGAAGAATACAAAGACTACTTCTGC ATCTCCAAATGGTACCTGAAGGAAGTTAAA CGCAAACCGTACAACCTGAAACTGGGTTGC AATTGGCAGTTCATCCCGAAAGACGAAGGT
Amended_Seq7      GTATTCGAAGAATACAAAGACTACTTCTGC ATCTCCAAATGGTACCTGAAGGAAGTTAAA CGCAAACCGTACAACCTGAAACTGGGTTGC AATTGGCAGTTCATCCCGAAAGACGAAGGT
Original_Fig4     GTATTCGAAGAATACAAAGACTACTTCTGC ATCTCCAAATGGTACCTGAAGGAAGTTAAA CGCAAACCGTACAACCTGAAACTGGGTTGC AATTGGCAGTTCATCCCGAAAGACGAAGGT


                          1321            1341
Original_Seq7     TGGACCGAATAGTAAGAATTC
Substitute_Seq7   TGGACCGAATAGTAAGAATTC
Amended_Seq7      TGGACCGAATAGTAAGAATTC
Original_Fig4     TGGACCGAATAGTAAGAATTC
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ALIGNMENT 2: SEQ ID NO:37

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             1                    30 31                   60 61                   90 91                  120
Original_Seq37   CTCGAGCCATGGCTCGTCTGCTGTCTACCT TCACTGAATACATCAAGAACATCATCAATA CCTCCATCCTGAACCTGCGCTACGAATCCA ATCACCTGATCGACCTGTCTCGCTACGCTT
Substitute_Seq37 CTCGAGCCATGGCTCGTCTGCTGTCTACCT TCACTGAATACATCAAGAACATCATCAATA CCTCCATCCTGAACCTGCGCTACGAATCCA ATCACCTGATCGACCTGTCTCGCTACGCTT
Amended_Seq37    CTCGAGCCATGGCTCGTCTGCTGTCTACCT TCACTGAATACATCAAGAACATCATCAATA CCTCCATCCTGAACCTGCGCTACGAATCCA ATCACCTGATCGACCTGTCTCGCTACGCTT
Pig2_'975_App    CTCGAGCCATGGCTCGTCTGCTGTCTACCT TCACTGAATACATCAAGAACATCATCAATA CCTCCATCCTGAACCTGCGCTACGAATCCA ATCACCTGATCGACCTGTCTCGCTACGCTT

             121                  150 151                 180 181                 210 211                 240
Original_Seq37   CCAAAATCAACATCGGTTCTAAAGTTAACT TCGATCCGATCGACAAGAATCAGATCCAGC TGTTCAATCTGGAATCTTCCAAAATCGAAG TTATCCTGAAGAATGCTATCGTATACAACT
Substitute_Seq37 CCAAAATCAACATCGGTTCTAAAGTTAACT TCGATCCGATCGACAAGAATCAGATCCAGC TGTTCAATCTGGAATCTTCCAAAATCGAAG TTATCCTGAAGAATGCTATCGTATACAACT
Amended_Seq37    CCAAAATCAACATCGGTTCTAAAGTTAACT TCGATCCGATCGACAAGAATCAGATCCAGC TGTTCAATCTGGAATCTTCCAAAATCGAAG TTATCCTGAAGAATGCTATCGTATACAACT
Pig2_'975_App    CCAAAATCAACATCGGTTCTAAAGTTAACT TCGATCCGATCGACAAGAATCAGATCCAGC TGTTCAATCTGGAATCTTCCAAAATCGAAG TTATCCTGAAGAATGCTATCGTATACAACT

             241                  270 271                 300 301                 330 331                 360
Original_Seq37   CTATGTACGAAAACTTCTCCACCTCCTTCT GGATCCGTATCCCGAAATACTTCAACTCCA TCTCTCTGAACAATGAATACACCATCATCA ACTGCATGGAAAACAATTCTGGTTGGAAAG
Substitute_Seq37 CTATGTACGAAAACTTCTCCACCTCCTTCT GGATCCGTATCCCGAAATACTTCAACTCCA TCTCTCTGAACAATGAATACACCATCATCA ACTGCATGGAAAACAATTCTGGTTGGAAAG
Amended_Seq37    CTATGTACGAAAACTTCTCCACCTCCTTCT GGATCCGTATCCCGAAATACTTCAACTCCA TCTCTCTGAACAATGAATACACCATCATCA ACTGCATGGAAAACAATTCTGGTTGGAAAG
Pig2_'975_App    CTATGTACGAAAACTTCTCCACCTCCTTCT GGATCCGTATCCCGAAATACTTCAACTCCA TCTCTCTGAACAATGAATACACCATCATCA ACTGCATGGAAAACAATTCTGGTTGGAAAG

             361                  390 391                 420 421                 450 451                 480
Original_Seq37   TATCTCTGAACTACGGTGAAATCATCTGGA CTCTGCAGGACACTCAGGAAATCAAACAGC GTGTTGTATTCAAATACTCTCAGATGATCA ACATCTCTGACTACATCAATCGCTGGATCT
Substitute_Seq37 TATCTCTGAACTACGGTGAAATCATCTGGA CTCTGCAGGACACTCAGGAAATCAAACAGC GTGTTGTATTCAAATACTCTCAGATGATCA ACATCTCTGACTACATCAATCGCTGGATCT
Amended_Seq37    TATCTCTGAACTACGGTGAAATCATCTGGA CTCTGCAGGACACTCAGGAAATCAAACAGC GTGTTGTATTCAAATACTCTCAGATGATCA ACATCTCTGACTACATCAATCGCTGGATCT
Pig2_'975_App    TATCTCTGAACTACGGTGAAATCATCTGGA CTCTGCAGGACACTCAGGAAATCAAACAGC GTGTTGTATTCAAATACTCTCAGATGATCA ACATCTCTGACTACATCAATCGCTGGATCT

             481                  510 511                 540 541                 570 571                 600
Original_Seq37   TCGTTACCATCACCAACAATCGTCTGAATA ACTCCAAAATCTACATCAACGGCCGTCTGA TCGACCAGAAACCGATCTCCAATCTGGGTA ACATCCACGGTTCTAATAACATCATGTTCA
Substitute_Seq37 TCGTTACCATCACCAACAATCGTCTGAATA ACTCCAAAATCTACATCAACGGCCGTCTGA TCGACCAGAAACCGATCTCCAATCTGGGTA ACATCCACGGTTCTAATAACATCATGTTCA
Amended_Seq37    TCGTTACCATCACCAACAATCGTCTGAATA ACTCCAAAATCTACATCAACGGCCGTCTGA TCGACCAGAAACCGATCTCCAATCTGGGTA ACATCCACGGTTCTAATAACATCATGTTCA
Pig2_'975_App    TCGTTACCATCACCAACAATCGTCTGAATA ACTCCAAAATCTACATCAACGGCCGTCTGA TCGACCAGAAACCGATCTCCAATCTGGGTA ACATCCACGGTTCTAATAACATCATGTTCA

             601                  630 631                 660 661                 690 691                 720
Original_Seq37   AACTGGACGGTTGTCGTGACACTCACCGCT ACATCTGGATCAAATACTTCAATCTGTTCG ACAAAGAACTGAACGAAAAAGAAATCAAAG ACCTGTACGACAACCAGTCCAATTCTGGTA
Substitute_Seq37 AACTGGACGGTTGTCGTGACACTCACCGCT ACATCTGGATCAAATACTTCAATCTGTTCG ACAAAGAACTGAACGAAAAAGAAATCAAAG ACCTGTACGACAACCAGTCCAATTCTGGTA
Amended_Seq37    AACTGGACGGTTGTCGTGACACTCACCGCT ACATCTGGATCAAATACTTCAATCTGTTCG ACAAAGAACTGAACGAAAAAGAAATCAAAG ACCTGTACGACAACCAGTCCAATTCTGGTA
Pig2_'975_App    AACTGGACGGTTGTCGTGACACTCACCGCT ACATCTGGATCAAATACTTCAATCTGTTCG ACAAAGAACTGAACGAAAAAGAAATCAAAG ACCTGTACGACAACCAGTCCAATTCTGGTA

             721                  750 751                 780 781                 810 811                 840
Original_Seq37   TCCTGAAAGACTTCTGGGGTGACTACCTGC AGTACGACAAACCGTACTACATGCTGAATC TGTACGATCCGAACAAATACGTTGACGTCA ACAATGTAGGTATCCGCGGTTACATGTACC
Substitute_Seq37 TCCTGAAAGACTTCTGGGGTGACTACCTGC AGTACGACAAACCGTACTACATGCTGAATC TGTACGATCCGAACAAATACGTTGACGTCA ACAATGTAGGTATCCGCGGTTACATGTACC
Amended_Seq37    TCCTGAAAGACTTCTGGGGTGACTACCTGC AGTACGACAAACCGTACTACATGCTGAATC TGTACGATCCGAACAAATACGTTGACGTCA ACAATGTAGGTATCCGCGGTTACATGTACC
Pig2_'975_App    TCCTGAAAGACTTCTGGGGTGACTACCTGC AGTACGACAAACCGTACTACATGCTGAATC TGTACGATCCGAACAAATACGTTGACGTCA ACAATGTAGGTATCCGCGGTTACATGTACC

             841                  870 871                 900 901                 930 931                 960
Original_Seq37   TGAAAGGTCCGCGTGGTTCTGTTATGACTA CCAACATCTACCTGAACTCTTCCCTGTACC GTGGTACCAAATTCATCATCAAGAAATACG CGTCTGGTAACAAGGACAATATGCTTCGCA
Substitute_Seq37 TGAAAGGTCCGCGTGGTTCTGTTATGACTA CCAACATCTACCTGAACTCTTCCCTGTACC GTGGTACCAAATTCATCATCAAGAAATACG CGTCTGGTAACAAGGACAATATCGTTCGCA
Amended_Seq37    TGAAAGGTCCGCGTGGTTCTGTTATGACTA CCAACATCTACCTGAACTCTTCCCTGTACC GTGGTACCAAATTCATCATCAAGAAATACG CGTCTGGTAACAAGGACAATATCGTTCGCA
Pig2_'975_App    TGAAAGGTCCGCGTGGTTCTGTTATGACTA CCAACATCTACCTGAACTCTTCCCTGTACC GTGGTACCAAATTCATCATCAAGAAATACG CGTCTGGTAACAAGGACAATATCGTTCGCA

             961                  990 991                1020 1021               1050 1051               1080
Original_Seq37   ACAATGATCGTGTATACATCAATGTTGTAG TTAAGAACAAAGAATACCGTCTGGCTACCA ATGCTTCTCAGGCTGGTGTAGAAAAGATCT TGTCTGCTCTGGAAATCCCGGACGTTGGTA
Substitute_Seq37 ACAATGATCGTGTATACATCAATGTTGTAG TTAAGAACAAAGAATACCGTCTGGCTACCA ATGCTTCTCAGGCTGGTGTAGAAAAGATCT TGTCTGCTCTGGAAATCCCGGACGTTGGTA
Amended_Seq37    ACAATGATCGTGTATACATCAATGTTGTAG TTAAGAACAAAGAATACCGTCTGGCTACCA ATGCTTCTCAGGCTGGTGTAGAAAAGATCT TGTCTGCTCTGGAAATCCCGGACGTTGGTA
Pig2_'975_App    ACAATGATCGTGTATACATCAATGTTGTAG TTAAGAACAAAGAATACCGTCTGGCTACCA ATGCTTCTCAGGCTGGTGTAGAAAAGATCT TGTCTGCTCTGGAAATCCCGGACGTTGGTA

             1081               1110 1111               1140 1141               1170 1171               1200
Original_Seq37   ATCTGTCTCAGGTAGTTGTAATGAAATCCA AGAACGACCAGGGTATCACTAACAAATGCA AAATGAATCTGCAGGACAACAATGGTAACG ATATCGGTTTCATCGGTTTCCACCAGTTCA
Substitute_Seq37 ATCTGTCTCAGGTAGTTGTAATGAAATCCA AGAACGACCAGGGTATCACTAACAAATGCA AAATGAATCTGCAGGACAACAATGGTAACG ATATCGGTTTCATCGGTTTCCACCAGTTCA
Amended_Seq37    ATCTGTCTCAGGTAGTTGTAATGAAATCCA AGAACGACCAGGGTATCACTAACAAATGCA AAATGAATCTGCAGGACAACAATGGTAACG ATATCGGTTTCATCGGTTTCCACCAGTTCA
Pig2_'975_App    ATCTGTCTCAGGTAGTTGTAATGAAATCCA AGAACGACCAGGGTATCACTAACAAATGCA AAATGAATCTGCAGGACAACAATGGTAACG ATATCGGTTTCATCGGTTTCCACCAGTTCA

             1201               1230 1231               1260 1261               1290 1291               1320
Original_Seq37   ACAATATCGCTAAACTGGTTGCTTCCAACT GGTACAATCGTCAGATCGAACGTTCCTCTC GCACTCTGGGTTGCTCTTGGGAGTTCATCC CGGTTGATGACGGTTGGGGTGAACGTCCGC
Substitute_Seq37 ACAATATCGCTAAACTGGTTGCTTCCAACT GGTACAATCGTCAGATCGAACGTTCCTCTC GCACTCTGGGTTGCTCTTGGGAGTTCATCC CGGTTGATGACGGTTGGGGTGAACGTCCGC
Amended_Seq37    ACAATATCGCTAAACTGGTTGCTTCCAACT GGTACAATCGTCAGATCGAACGTTCCTCTC GCACTCTGGGTTGCTCTTGGGAGTTCATCC CGGTTGATGACGGTTGGGGTGAACGTCCGC
Pig2_'975_App    ACAATATCGCTAAACTGGTTGCTTCCAACT GGTACAATCGTCAGATCGAACGTTCCTCTC GCACTCTGGGTTGCTCTTGGGAGTTCATCC CGGTTGATGACGGTTGGGGTGAACGTCCGC

             1321            1338
Original_Seq37   TGTAACCCGGGAAAGCTT
Substitute_Seq37 TGTAACCCGGGAAAGCTT
Amended_Seq37    TGTAACCCGGGAAAGCTT
Pig2_'975_App    TGTAACCCGGGAAAGCTT
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ALIGNMENT 3: SEQ ID NO:39

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                  1                              30 31                             60 61                             90 91                            120
Original_Seq39    ATGGC...CAACAAATACAATTCCGAAATC  CTGAACAATATCATCCTGAACCTGCGTTAC  AAAGACAACAATCTGATCGATCTGTCTGGT  TACGGTGCTAAAGTTGAAGTATACGACGGT
Substitute_Seq39  ATGGC...CAACAAATACAATTCCGAAATC  CTGAACAATATCATCCTGAACCTGCGTTAC  AAAGACAACAATCTGATCGATCTGTCTGGT  TACGGTGCTAAAGTTGAAGTATACGACGGT
Amended_Seq39     ATGGC[TTT]CAACAAATACAATTCCGAAATC  CTGAACAATATCATCCTGAACCTGCGTTAC  AAAGACAACAATCTGATCGATCTGTCTGGT  TACGGTGCTAAAGTTGAAGTATACGACGGT
Fig4_'975_App     ATGGC[TTT]CAACAAATACAATTCCGAAATC  CTGAACAATATCATCCTGAACCTGCGTTAC  AAAGACAACAATCTGATCGATCTGTCTGGT  TACGGTGCTAAAGTTGAAGTATACGACGGT

                  121                            150 151                           180 181                           210 211                           240
Original_Seq39    GTTGAACTGAATGACAAGAACCAGTTCAAA  CTGACCTCTTCCGCTAACTCTAAGATCCGT  GTTACTCAGAATCAGAACATCATCTTCAAC  TCCGTATTCCTGGACTTCTCTCTGTTTCCTTC
Substitute_Seq39  GTTGAACTGAATGACAAGAACCAGTTCAAA  CTGACCTCTTCCGCTAACTCTAAGATCCGT  GTTACTCAGAATCAGAACATCATCTTCAAC  TCCGTATTCCTGGACTTCTCTCTGTTTCCTTC
Amended_Seq39     GTTGAACTGAATGACAAGAACCAGTTCAAA  CTGACCTCTTCCGCTAACTCTAAGATCCGT  GTTACTCAGAATCAGAACATCATCTTCAAC  TCCGTATTCCTGGACTTCTCTCTGTTTCCTTC
Fig4_'975_App     GTTGAACTGAATGACAAGAACCAGTTCAAA  CTGACCTCTTCCGCTAACTCTAAGATCCGT  GTTACTCAGAATCAGAACATCATCTTCAAC  TCCGTATTCCTGGACTTCTCTCTGTTTCCTTC

                  241                            270 271                           300 301                           330 331                           360
Original_Seq39    TGGATCCGTATCCCGAAATACAAGAACGAC  GGTATCCAGAATTACATCCACAATGAATAC  ACCATCATCAACTGCATGAAGAATAACTCT  GGTTGGAAGATCTCCATCCGCGGTAACCGT
Substitute_Seq39  TGGATCCGTATCCCGAAATACAAGAACGAC  GGTATCCAGAATTACATCCACAATGAATAC  ACCATCATCAACTGCATGAAGAATAACTCT  GGTTGGAAGATCTCCATCCGCGGTAACCGT
Amended_Seq39     TGGATCCGTATCCCGAAATACAAGAACGAC  GGTATCCAGAATTACATCCACAATGAATAC  ACCATCATCAACTGCATGAAGAATAACTCT  GGTTGGAAGATCTCCATCCGCGGTAACCGT
Fig4_'975_App     TGGATCCGTATCCCGAAATACAAGAACGAC  GGTATCCAGAATTACATCCACAATGAATAC  ACCATCATCAACTGCATGAAGAATAACTCT  GGTTGGAAGATCTCCATCCGCGGTAACCGT

                  361                            390 391                           420 421                           450 451                           480
Original_Seq39    ATCATCTGGACTCTGATCGATATCAACGGT  AAGACCAAATCTGTATTCTTCGAATACAAC  ATCCGTGAAGACATCTCTGAATACATCAAT  CGCTGGTTCTTCGTTACCATCACCAATAAC
Substitute_Seq39  ATCATCTGGACTCTGATCGATATCAACGGT  AAGACCAAATCTGTATTCTTCGAATACAAC  ATCCGTGAAGACATCTCTGAATACATCAAT  CGCTGGTTCTTCGTTACCATCACCAATAAC
Amended_Seq39     ATCATCTGGACTCTGATCGATATCAACGGT  AAGACCAAATCTGTATTCTTCGAATACAAC  ATCCGTGAAGACATCTCTGAATACATCAAT  CGCTGGTTCTTCGTTACCATCACCAATAAC
Fig4_'975_App     ATCATCTGGACTCTGATCGATATCAACGGT  AAGACCAAATCTGTATTCTTCGAATACAAC  ATCCGTGAAGACATCTCTGAATACATCAAT  CGCTGGTTCTTCGTTACCATCACCAATAAC

                  481                            510 511                           540 541                           570 571                           600
Original_Seq39    CTGAACAATGCTAAAATCTACATCAACGGT  AAACTGGAATCTAATACCGACATCAAAGAC  ATCCGTGAAGTTATCGCTAACGGTGAAATC  ATCTTCAAACTGGACGGTGACATCGATCGT
Substitute_Seq39  CTGAACAATGCTAAAATCTACATCAACGGT  AAACTGGAATCTAATACCGACATCAAAGAC  ATCCGTGAAGTTATCGCTAACGGTGAAATC  ATCTTCAAACTGGACGGTGACATCGATCGT
Amended_Seq39     CTGAACAATGCTAAAATCTACATCAACGGT  AAACTGGAATCTAATACCGACATCAAAGAC  ATCCGTGAAGTTATCGCTAACGGTGAAATC  ATCTTCAAACTGGACGGTGACATCGATCGT
Fig4_'975_App     CTGAACAATGCTAAAATCTACATCAACGGT  AAACTGGAATCTAATACCGACATCAAAGAC  ATCCGTGAAGTTATCGCTAACGGTGAAATC  ATCTTCAAACTGGACGGTGACATCGATCGT

                  601                            630 631                           660 661                           690 691                           720
Original_Seq39    ACCCAGTTCATCTGGATGAAATACTTCTCC  ATCTTCAACACCGAACTGTCTCAGTCCAAT  ATCGAAGAACGGTACAAGATCCAGTCTTAC  TCCGAATACCTGAAAGACTTCTGGGGTAAT
Substitute_Seq39  ACCCAGTTCATCTGGATGAAATACTTCTCC  ATCTTCAACACCGAACTGTCTCAGTCCAAT  ATCGAAGAACGGTACAAGATCCAGTCTTAC  TCCGAATACCTGAAAGACTTCTGGGGTAAT
Amended_Seq39     ACCCAGTTCATCTGGATGAAATACTTCTCC  ATCTTCAACACCGAACTGTCTCAGTCCAAT  ATCGAAGAACGGTACAAGATCCAGTCTTAC  TCCGAATACCTGAAAGACTTCTGGGGTAAT
Fig4_'975_App     ACCCAGTTCATCTGGATGAAATACTTCTCC  ATCTTCAACACCGAACTGTCTCAGTCCAAT  ATCGAAGAACGGTACAAGATCCAGTCTTAC  TCCGAATACCTGAAAGACTTCTGGGGTAAT

                  721                            750 751                           780 781                           810 811                           840
Original_Seq39    CCGCTGATGTACAACAAAGAATACTATATG  TTCAATGCTGGTAACAAGAACTCTTACATC  AAACTGAAGAAAGACTCTCCGGTTGGTGAA  [G]TCCTGACTCGTTCCAAATACAACCAGAAC
Substitute_Seq39  CCGCTGATGTACAACAAAGAATACTATATG  TTCAATGCTGGTAACAAGAACTCTTACATC  AAACTGAAGAAAGACTCTCCGGTTGGTGAA  [A]TCCTGACTCGTTCCAAATACAACCAGAAC
Amended_Seq39     CCGCTGATGTACAACAAAGAATACTATATG  TTCAATGCTGGTAACAAGAACTCTTACATC  AAACTGAAGAAAGACTCTCCGGTTGGTGAA  [A]TCCTGACTCGTTCCAAATACAACCAGAAC
Fig4_'975_App     CCGCTGATGTACAACAAAGAATACTATATG  TTCAATGCTGGTAACAAGAACTCTTACATC  AAACTGAAGAAAGACTCTCCGGTTGGTGAA  [A]TCCTGACTCGTTCCAAATACAACCAGAAC

                  841                            870 871                           900 901                           930 931                           960
Original_Seq39    TCTAAATACATCAACTACCGCGACCTGTAC  ATCGGTGAAAAGTTCATCATCCGTCGCAAA  TCTAACTCTCAGTCCATCAATGA[G]GACATC  GTACGTAAAGAAGACTACATCTACCTGGAC
Substitute_Seq39  TCTAAATACATCAACTACCGCGACCTGTAC  ATCGGTGAAAAGTTCATCATCCGTCGCAAA  TCTAACTCTCAGTCCATCAATGA[T]GACATC  GTACGTAAAGAAGACTACATCTACCTGGAC
Amended_Seq39     TCTAAATACATCAACTACCGCGACCTGTAC  ATCGGTGAAAAGTTCATCATCCGTCGCAAA  TCTAACTCTCAGTCCATCAATGA[T]GACATC  GTACGTAAAGAAGACTACATCTACCTGGAC
Fig4_'975_App     TCTAAATACATCAACTACCGCGACCTGTAC  ATCGGTGAAAAGTTCATCATCCGTCGCAAA  TCTAACTCTCAGTCCATCAATGA[T]GACATC  GTACGTAAAGAAGACTACATCTACCTGGAC

                  961                            990 991                           1020 1021                         1050 1051                          1080
Original_Seq39    TTCTTCAACCTGAATCAG[G]AATGGCGTGTA  TACACCTACAAGTACTTCAAGAAAGAAGAA  GAAAAGCTTTTCCTGGCTCCGATCTCTGAT  TCCGACGAACTCTACAACACCATCCAGATC
Substitute_Seq39  TTCTTCAACCTGAATCAG[G]AATGGCGTGTA  TACACCTACAAGTACTTCAAGAAAGAAGAA  GAAAAGCTTTTCCTGGCTCCGATCTCTGAT  TCCGACGAACTCTACAACACCATCCAGATC
Amended_Seq39     TTCTTCAACCTGAATCAG[G]AATGGCGTGTA  TACACCTACAAGTACTTCAAGAAAGAAGAA  GAAAAGCTTTTCCTGGCTCCGATCTCTGAT  TCCGACGAACTCTACAACACCATCCAGATC
Fig4_'975_App     TTCTTCAACCTGAATCAG[G]AATGGCGTGTA  TACACCTACAAGTACTTCAAGAAAGAAGAA  GAAAAGCTTTTCCTGGCTCCGATCTCTGAT  TCCGACGAACTCTACAACACCATCCAGATC

                  1081                           1110 1111                          1140 1141                         1170 1171                          1200
Original_Seq39    AAAGAATACGACGAACAGCCGACCTACTCT  TGCCAGCTGCTGTTCAAGAAAGATGAAGAA  TCTACTGACGAAATCGGTCTGATCGGTATC  CACCGTTTCTACGAATCTGGTATCGTATTC
Substitute_Seq39  AAAGAATACGACGAACAGCCGACCTACTCT  TGCCAGCTGCTGTTCAAGAAAGATGAAGAA  TCTACTGACGAAATCGGTCTGATCGGTATC  CACCGTTTCTACGAATCTGGTATCGTATTC
Amended_Seq39     AAAGAATACGACGAACAGCCGACCTACTCT  TGCCAGCTGCTGTTCAAGAAAGATGAAGAA  TCTACTGACGAAATCGGTCTGATCGGTATC  CACCGTTTCTACGAATCTGGTATCGTATTC
Fig4_'975_App     AAAGAATACGACGAACAGCCGACCTACTCT  TGCCAGCTGCTGTTCAAGAAAGATGAAGAA  TCTACTGACGAAATCGGTCTGATCGGTATC  CACCGTTTCTACGAATCTGGTATCGTATTC

                  1201                           1230 1231                          1260 1261                         1290 1291                          1320
Original_Seq39    GAAGAATACAAAGACT[C]CTTCTGCATCTCC  AAATGGTACCTGAAGGAAGTTAAACGCAAA  CCGTACAACCTGAAACTGGGTTGCAATTGG  CAGTTCATCCCGAAAGACGAAGGTTGGACC
Substitute_Seq39  GAAGAATACAAAGACT[A]CTTCTGCATCTCC  AAATGGTACCTGAAGGAAGTTAAACGCAAA  CCGTACAACCTGAAACTGGGTTGCAATTGG  CAGTTCATCCCGAAAGACGAAGGTTGGACC
Amended_Seq39     GAAGAATACAAAGACT[A]CTTCTGCATCTCC  AAATGGTACCTGAAGGAAGTTAAACGCAAA  CCGTACAACCTGAAACTGGGTTGCAATTGG  CAGTTCATCCCGAAAGACGAAGGTTGGACC
Fig4_'975_App     GAAGAATACAAAGACT[A]CTTCTGCATCTCC  AAATGGTACCTGAAGGAAGTTAAACGCAAA  CCGTACAACCTGAAACTGGGTTGCAATTGG  CAGTTCATCCCGAAAGACGAAGGTTGGACC

                  1321                           1350 1351
Original_Seq39    GAATAGTAACCTCTAGAGTCGAGGCCTGCA  G
Substitute_Seq39  GAATAGTAACCTCTAGAGTCGAGGCCTGCA  G
Amended_Seq39     GAATAGTAACCTCTAGAGTCGAGGCCTGCA  G
Fig4_'975_App     GAATAGTAACCTCTAGAGTCGAGGCCTGCA  G
```

ALIGNMENT 4:   SEQ ID NO:40

```
              1                   30 31                  60 61                  90 91                  120
Original_Seq40   -----------------------  ------------------------  ------------------------  ------------------------
Substitute_Seq40 -----------------------  ------------------------  ------------------------  ------------------------
Amended_Seq40    -----------------------  ------------------------  ------------------------  ------------------------
Whelan_M81186    MPVTINNFNYNDPIDNNNIIMMEPPFARGT GRYYKAFKITDRIWIIPERYTFGYKPEDFN KSSGIFNRDVCEYYDPDYLNTNDKKNIFLQ TMIKLFNRIKSKPLGEKLLEMIINGIPYLG


              121                 150 151                 180 181                 210 211                 240
Original_Seq40   -----------------------  ------------------------  ------------------------  ------------------------
Substitute_Seq40 -----------------------  ------------------------  ------------------------  ------------------------
Amended_Seq40    -----------------------  ------------------------  ------------------------  ------------------------
Whelan_M81186    DRRVPLEEFNTNIASVTVNKLISNPGEVER KKGIFANLIIFGPGPVLNENETIDIGIQNH PASREGFGGIMQMKFCPEYVSVFNNVQENK GASIFNRRGYFSDPALILMHELIHVLHGLY


              241                 270 271                 300 301                 330 331                 360
Original_Seq40   -----------------------  ------------------------  ------------------------  ------------------------
Substitute_Seq40 -----------------------  ------------------------  ------------------------  ------------------------
Amended_Seq40    -----------------------  ------------------------  ------------------------  ------------------------
Whelan_M81186    GIKVDDLPIVPNEKKPFMQSTDAIQAEELY TPGGQDPSIITPSTDKSIYDKVLQNFRGIV DRLNKVLVCISDPNININIYKNKFKDKYKF VEDSEGKYSIDVESFDKLYKSLMFGFTETN


              361                 390 391                 420 421                 450 451                 480
Original_Seq40   -----------------------  ------------------------  ------------------------  ------------------------
Substitute_Seq40 -----------------------  ------------------------  ------------------------  ------------------------
Amended_Seq40    -----------------------  ------------------------  ------------------------  ------------------------
Whelan_M81186    IAENYKIKTRASYFSDSLPPVKIKNLLDNE IYTIEEGFNISDKDMEKEYRGQNKAINKQA YEEISKEHLAVYKIQMCKSVKAPGICIDVD NEDLFPIADKNSFSDDLSKNERIEYNTQSN


              481                 510 511                 540 541                 570 571                 600
Original_Seq40   -----------------------  ------------------------  ------------------------  ------------------------
Substitute_Seq40 -----------------------  ------------------------  ------------------------  ------------------------
Amended_Seq40    -----------------------  ------------------------  ------------------------  ------------------------
Whelan_M81186    YIENDPPINELILDTDLISKIELPSENTES LTDPNVDVPVYEKQPAIKKIFTDENTIPQY LYSQTFPLDIRDISLTSSPDDALLFSNKVY SFFSMDYIKTANKVVEAGLFAGWVKQIVND


              601                 630 631                 660 661                 690 691                 720
Original_Seq40   -----------------------  ------------------------  ------------------------  ------------------------
Substitute_Seq40 -----------------------  ------------------------  ------------------------  ------------------------
Amended_Seq40    -----------------------  ------------------------  ------------------------  ------------------------
Whelan_M81186    FVIEANKSNTMDKIADISLIVPYIGLALNV GNETAKGNFENAFEIAGASILLEFIPELLI PVVGAFLLESYIDNKNKIIKTIDNALTKRN EKWSDMYGLIVAQWLSTVNTQFYTIKEGMY


              721                 750 751                 780 781                 810 811                 840
Original_Seq40   -----------------------  ------------------------  ------------------------  ------------------------
Substitute_Seq40 -----------------------  ------------------------  ------------------------  ------------------------
Amended_Seq40    -----------------------  ------------------------  ------------------------  ------------------------
Whelan_M81186    KALNYQAQALEEIIKYRYNIYSEKEKSNIN IDPNDINSKLNEGINQAIDNINNFINGCSV SYLMKKMIPLAVEKLLDFDNTLKKNLLNYI DENKLYLIGSAEYEKSKVNKYLKTIMPPDL


              841                 870 871                 900 901                 930 931                 960
Original_Seq40   ------------FNKYNSEILNNIILNLRY KDNNLIDLSGYGAKVEVYDGVELNDKNQFK LTSSANSKIRVTQNQNIIFNSVFLDFSVSP WIRIPKYKNDGIQNYIHNEYTIINCMKNNS
Substitute_Seq40 ------------FNKYNSEILNNIILNLRY KDNNLIDLSGYGAKVEVYDGVELNDKNQFK LTSSANSKIRVTQNQNIIFNSVFLDFSVSP WIRIPKYKNDGIQNYIHNEYTIINCMKNNS
Amended_Seq40    ------------FNKYNSEILNNIILNLRY KDNNLIDLSGYGAKVEVYDGVELNDKNQFK LTSSANSKIRVTQNQNIIFNSVFLDFSVSP WIRIPKYKNDGIQNYIHNEYTIINCMKNNS
Whelan_M81186    SIYTNDTILIEMFNKYNSEILNNIILNLRY KDNNLIDLSGYGAKVEVYDGVELNDKNQFK LTSSANSKIRVTQNQNIIFNSVFLDFSVSP WIRIPKYKNDGIQNYIHNEYTIINCMKNNS


              961                 990 991                1020 1021                1050 1051                1080
Original_Seq40   GWKISIRGNRIWTLIDINGKTKSVFPEYN IREDISEYINRWFFVTITNNLNNAKIYING KLESNTDIKDIREVIANGEIIFKLDGDIDR TQFIWMKYFSIFNTELSQSNIEERYKIQSY
Substitute_Seq40 GWKISIRGNRIWTLIDINGKTKSVFPEYN IREDISEYINRWFFVTITNNLNNAKIYING KLESNTDIKDIREVIANGEIIFKLDGDIDR TQFIWMKYFSIFNTELSQSNIEERYKIQSY
Amended_Seq40    GWKISIRGNRIWTLIDINGKTKSVFPEYN IREDISEYINRWFFVTITNNLNNAKIYING KLESNTDIKDIREVIANGEIIFKLDGDIDR TQFIWMKYFSIFNTELSQSNIEERYKIQSY
Whelan_M81186    GWKISIRGNRIWTLIDINGKTKSVFPEYN IREDISEYINRWFFVTITNNLNNAKIYING KLESNTDIKDIREVIANGEIIFKLDGDIDR TQFIWMKYFSIFNTELSQSNIEERYKIQSY


              1081                1110 1111                1140 1141                1170 1171                1200
Original_Seq40   SEYLKDFWGNPLMYNKEYYMFNAGNKNSYI KLKKDSPVGEILTRSKYNQNSKYINYRDLY IGEKFIIRRKSNSQSINDDIVRKEDYIYLD FFNLNQEDRVYTYKFPKKEEEKLFLAPISD
Substitute_Seq40 SEYLKDFWGNPLMYNKEYYMFNAGNKNSYI KLKKDSPVGEILTRSKYNQNSKYINYRDLY IGEKFIIRRKSNSQSINDDIVRKEDYIYLD FFNLNQEDRVYTYKFPKKEEEKLFLAPISD
Amended_Seq40    SEYLKDFWGNPLMYNKEYYMFNAGNKNSYI KLKKDSPVGEILTRSKYNQNSKYINYRDLY IGEKFIIRRKSNSQSINDDIVRKEDYIYLD FFNLNQEDRVYTYKFPKKEEEKLFLAPISD
Whelan_M81186    SEYLKDFWGNPLMYNKEYYMFNAGNKNSYI KLKKDSPVGEILTRSKYNQNSKYINYRDLY IGEKFIIRRKSNSQSINDDIVRKEDYIYLD FFNLNQEDRVYTYKFPKKEEEKLFLAPISD


              1201                1230 1231                1260 1261                1290 1291
Original_Seq40   SDEPYNTIQIKEYDEQPTYSCQLLFKKDEE STDEIGLIGIHRFYESGIVFEEYKDYFCIS KWYLKEVKRKPYNLKLGCNWQFIPKDEGWT E
Substitute_Seq40 SDEPYNTIQIKEYDEQPTYSCQLLFKKDEE STDEIGLIGIHRFYESGIVFEEYKDYFCIS KWYLKEVKRKPYNLKLGCNWQFIPKDEGWT E
Amended_Seq40    SDEPYNTIQIKEYDEQPTYSCQLLFKKDEE STDEIGLIGIHRFYESGIVFEEYKDYFCIS KWYLKEVKRKPYNLKLGCNWQFIPKDEGWT E
Whelan_M81186    SDEPYNTIQIKEYDEQPTYSCQLLFKKDEE STDEIGLIGIHRFYESGIVFEEYKDYFCIS KWYLKEVKRKPYNLKLGCNWQFIPKDEGWT E
```

ALIGNMENT 5: SEQ ID NO:41

```
                      1              30 31            60 61            90 91           120
Original_Seq41        --------------------------------------------------------------------------------
Substitute_Seq41      --------------------------------------------------------------------------------
Amended_Seq41         --------------------------------------------------------------------------------
Thompson_X52066       MQFVNKQFNYKDPVNGVDIAYIKIPNVGQM QPVKAFKIHNKIWVIPERDTFTNPEEGDLN PPPEAKQVPVSYYDSTYLSTDNEKDNYLKG VTKLFERIYSTDLGRMLLTSIVRGIPFWGG


                      121           150 151          180 181          210 211          240
Original_Seq41        --------------------------------------------------------------------------------
Substitute_Seq41      --------------------------------------------------------------------------------
Amended_Seq41         --------------------------------------------------------------------------------
Thompson_X52066       STIDTELKVIDTNCINVIQPDGSYRSEELN LVIIGPSADIIQPECKSFGHEVLNLTRNGY GSTQYIRFSPDFTFGFEESLEVDTNPLLGA GKFATDPAVTLAHELIHAGHRLYGIAINPN


                      241           270 271          300 301          330 331          360
Original_Seq41        --------------------------------------------------------------------------------
Substitute_Seq41      --------------------------------------------------------------------------------
Amended_Seq41         --------------------------------------------------------------------------------
Thompson_X52066       RVFKVNTNAYYEMSGLEVSFEELRTFGGHD AKFIDSLQENEFRLYYYNKPKDIASTLNKA KSIVGTTASLQYMKNVFKEKYLLSEDTSGK FSVDKLKFDKLYKMLTEIYTEDNFVKFPKV


                      361           390 391          420 421          450 451          480
Original_Seq41        ----------------------------- ------------------------------ --------------------------AL NDLCIKVNNWDLFFSPSEDNFTNDLNKGEE
Substitute_Seq41      ----------------------------- ------------------------------ --------------------------AL NDLCIKVNNWDLFFSPSEDNFTNDLNKGEE
Amended_Seq41         ----------------------------- ------------------------------ --------------------------AL NDLCIKVNNWDLFFSPSEDNFTNDLNKGEE
Thompson_X52066       LNRKTYLNFDKAVFKINIVPKVNYTIYDGP NLRNTNLAANFNGQNTEINNMMNFTKLKNFT GLFEFYKLLCVRGIITSKTKSLDKGYNKAL NDLCIKVNNWDLFFSPSEDNFTNDLNKGEE


                      481           510 511          540 541          570 571          600
Original_Seq41        ITSDTNIEAAEENISLDLIQQYYLTFNFDN EPENISIENLSSDIIGQLELMPNIERFPNG KKYELDKYTMFHYLRAQEFEHGKSRIALTN SVNEALLNPSRVYTFFSSDYVKKVNKATEA
Substitute_Seq41      ITSDTNIEAAEENISLDLIQQYYLTFNFDN EPENISIENLSSDIIGQLELMPNIERFPNG KKYELDKYTMFHYLRAQEFEHGKSRIALTN SVNEALLNPSRVYTFFSSDYVKKVNKATEA
Amended_Seq41         ITSDTNIEAAEENISLDLIQQYYLTFNFDN EPENISIENLSSDIIGQLELMPNIERFPNG KKYELDKYTMFHYLRAQEFEHGKSRIALTN SVNEALLNPSRVYTFFSSDYVKKVNKATEA
Thompson_X52066       ITSDTNIEAAEENISLDLIQQYYLTFNFDN EPENISIENLSSDIIGQLELMPNIERFPNG KKYELDKYTMFHYLRAQEFEHGKSRIALTN SVNEALLNPSRVYTFFSSDYVKKVNKATEA


                      601           630 631          660 661          690 691          720
Original_Seq41        AMPLGWVEQLVYDFTDETSEVSTTDKIADI TIIIPYIGPALNIGMLYKDDFVGALIFSG AVILLEFIPEIAIPVLGTFALVSYIANKVL TVQTIDNALSKRNEKWDEVYKYIVTNWLAK
Substitute_Seq41      AMPLGWVEQLVYDFTDETSEVSTTDKIADI TIIIPYIGPALNIGMLYKDDFVGALIFSG AVILLEFIPEIAIPVLGTFALVSYIANKVL TVQTIDNALSKRNEKWDEVYKYIVTNWLAK
Amended_Seq41         AMPLGWVEQLVYDFTDETSEVSTTDKIADI TIIIPYIGPALNIGMLYKDDFVGALIFSG AVILLEFIPEIAIPVLGTFALVSYIANKVL TVQTIDNALSKRNEKWDEVYKYIVTNWLAK
Thompson_X52066       AMPLGWVEQLVYDFTDETSEVSTTDKIADI TIIIPYIGPALNIGMLYKDDFVGALIFSG AVILLEFIPEIAIPVLGTFALVSYIANKVL TVQTIDNALSKRNEKWDEVYKYIVTNWLAK


                      721           750 751          780 781          810 811          840
Original_Seq41        VNTQIDLIRKKMKEALENQAEATKAIINYQ YNQYTEEEKNNINFNIDDLSSKLNESINKA MININKFLNQCSVSYLMNSMIPYGVKRLED FDASLKDALLKYIRDNYGTLIGQVDRLKDK
Substitute_Seq41      VNTQIDLIRKKMKEALENQAEATKAIINYQ YNQYTEEEKNNINFNIDDLSSKLNESINKA MININKFLNQCSVSYLMNSMIPYGVKRLED FDASLKDALLKYIRDNYGTLIGQVDRLKDK
Amended_Seq41         VNTQIDLIRKKMKEALENQAEATKAIINYQ YNQYTEEEKNNINFNIDDLSSKLNESINKA MININKFLNQCSVSYLMNSMIPYGVKRLED FDASLKDALLKYIRDNYGTLIGQVDRLKDK
Thompson_X52066       VNTQIDLIRKKMKEALENQAEATKAIINYQ YNQYTEEEKNNINFNIDDLSSKLNESINKA MININKFLNQCSVSYLMNSMIPYGVKRLED FDASLKDALLKYIRDNYGTLIGQVDRLKDK


                      841           870 871          900 901          930 931          960
Original_Seq41        VNNTLSTDIPFQLSKYVDNQRLLSTFTEYI KNIINTSILNLRYESNHLIDLSRYASKINI GSKVNFDPIDKNQIQLFNLESSKIEVILKN AIVYNSMYENFSTSPWIRIPKYFNSISLNN
Substitute_Seq41      VNNTLSTDIPFQLSKYVDNQRLLSTFTEYI KNIINTSILNLRYESNHLIDLSRYASKINI GSKVNFDPIDKNQIQLFNLESSKIEVILKN AIVYNSMYENFSTSPWIRIPKYFNSISLNN
Amended_Seq41         VNNTLSTDIPFQLSKYVDNQRLLSTFTEYI KNIINTSILNLRYESNHLIDLSRYASKINI GSKVNFDPIDKNQIQLFNLESSKIEVILKN AIVYNSMYENFSTSPWIRIPKYFNSISLNN
Thompson_X52066       VNNTLSTDIPFQLSKYVDNQRLLSTFTEYI KNIINTSILNLRYESNHLIDLSRYASKINI GSKVNFDPIDKNQIQLFNLESSKIEVILKN AIVYNSMYENFSTSPWIRIPKYFNSISLNN


                      961           990 991         1020 1021         1050 1051         1080
Original_Seq41        EYTIINCMENNSGWKVSLNYGEIIWTLQDT QEIKQRVVFKYSQMINISDYINRWIFVTIT NNRLNNSKIYINGRLIDQKPISNLGNIHA SNNIMFKLDGCRDTHRYIWIKYFNLFDKEL
Substitute_Seq41      EYTIINCMENNSGWKVSLNYGEIIWTLQDT QEIKQRVVFKYSQMINISDYINRWIFVTIT NNRLNNSKIYINGRLIDQKPISNLGNIHA SNNIMFKLDGCRDTHRYIWIKYFNLFDKEL
Amended_Seq41         EYTIINCMENNSGWKVSLNYGEIIWTLQDT QEIKQRVVFKYSQMINISDYINRWIFVTIT NNRLNNSKIYINGRLIDQKPISNLGNIHA SNNIMFKLDGCRDTHRYIWIKYFNLFDKEL
Thompson_X52066       EYTIINCMENNSGWKVSLNYGEIIWTLQDT QEIKQRVVFKYSQMINISDYINRWIFVTIT NNRLNNSKIYINGRLIDQKPISNLGNIHA SNNIMFKLDGCRDTHRYIWIKYFNLFDKEL


                      1081         1110 1111         1140 1141         1170 1171         1200
Original_Seq41        NEKEIKDLYDNQSNSGILKDFWGDYLQYDK PYYMILLYDPNKYVDVNNVGIRGYMYLKGP RGSVMTTNIYLNSSLYRGTKFIIKKASGN KDNIVRNNDRVYINVVVKNKEYRLATNASQ
Substitute_Seq41      NEKEIKDLYDNQSNSGILKDFWGDYLQYDK PYYMILLYDPNKYVDVNNVGIRGYMYLKGP RGSVMTTNIYLNSSLYRGTKFIIKKASGN KDNIVRNNDRVYINVVVKNKEYRLATNASQ
Amended_Seq41         NEKEIKDLYDNQSNSGILKDFWGDYLQYDK PYYMLNLYDPNKYVDVNNVGIRGYMYLKGP RGSVMTTNIYLNSSLYRGTKFIIKKASGN KDNIVRNNDRVYINVVVKNKEYRLATNASQ
Thompson_X52066       NEKEIKDLYDNQSNSGILKDFWGDYLQYDK PYYMLNLYDPNKYVDVNNVGIRGYMYLKGP RGSVMTTNIYLNSSLYRGTKFIIKKASGN KDNIVRNNDRVYINVVVKNKEYRLATNASQ


                      1201         1230 1231         1260 1261         1290 1297
Original_Seq41        AGVEKILSALEIPDVGNLSQVVVMKSKNDQ GITNKCKMNLQDNNGNDIGFIGFHQFNNIA KLVASNWYNRQTERSSRTLGCSWEFIPVDD GWGERPL
Substitute_Seq41      AGVEKILSALEIPDVGNLSQVVVMKSKNDQ GITNKCKMNLQDNNGNDIGFIGFHQFNNIA KLVASNWYNRQTERSSRTLGCSWEFIPVDD GWGERPL
Amended_Seq41         AGVEKILSALEIPDVGNLSQVVVMKSKNDQ GITNKCKMNLQDNNGNDIGFIGFHQFNNIA KLVASNWYNRQTERSSRTLGCSWEFIPVDD GWGERPL
Thompson_X52066       AGVEKILSALEIPDVGNLSQVVVMKSKNDQ GITNKCKMNLQDNNGNDIGFIGFHQFNNIA KLVASNWYNRQTERSSRTLGCSWEFIPVDD GWGERPL
```

ALIGNMENT 6: SEQ ID NO:42

```
            1                 30 31                60 61                90 91               120
Original_Seq42   ------------------------  -------------------------  -------------------------  -------------------------
Substitute_Seq42 ------------------------  -------------------------  -------------------------  -------------------------
Amended_Seq42    ------------------------  -------------------------  -------------------------  -------------------------
Whelan_M81186    MPVTINNFNYNDPIDNNNIIMMEPPFARGT GRYYKAFKITDRIWIIPERYTFGYKPEDPN KSSGIFNRDVCEYYDPDYLNTNDKKNIFLQ TMIKLFNRIKSKPLGEKLLEMIINGIPYLG
```

```
            121              150 151              180 181              210 211              240
Original_Seq42   ------------------------  -------------------------  -------------------------  -------------------------
Substitute_Seq42 ------------------------  -------------------------  -------------------------  -------------------------
Amended_Seq42    ------------------------  -------------------------  -------------------------  -------------------------
Whelan_M81186    DRRVPLEEFNTNIASVTVNKLISNPGEVER KKGIFANLIIFGPGPVLNENETIDIGIQNH FASREGFGGIMQMKFCPEYVSVPNNVQENK GASIFNRRGYFSDPALILMHELIHVLHGLY
```

```
            241              270 271              300 301              330 331              360
Original_Seq42   ------------------------  -------------------------  -------------------------  -------------------------
Substitute_Seq42 ------------------------  -------------------------  -------------------------  -------------------------
Amended_Seq42    ------------------------  -------------------------  -------------------------  -------------------------
Whelan_M81186    GIKVDDLPIVPNEKKPFMQSTDAIQAEELY TFGGQDPSIITPSTDKSIYDKVLQNPRGIV DRLNKVLVCISDPNININIYKNKPKDKYKF VEDSEGKYSIDVESFDKLYKSLMFGFTETN
```

```
            361              390 391              420 421              450 451              480
Original_Seq42   ------------------------  -------------------------  --------------------APGICIDVD NEDLFPIADKNSFSDDLSKNERIEYNTQSN
Substitute_Seq42 ------------------------  -------------------------  --------------------APGICIDVD NEDLFPIADKNSPDDLSKNERIEYNTQSN
Amended_Seq42    ------------------------  -------------------------  --------------------APGICIDVD NEDLFPIADKNSPDDLSKNERIEYNTQSN
Whelan_M81186    IAENYKIKTRASYFSDSLPPVKIKNLLDNE IYTIEEGFNISDKDMEKEYRGQNKAINKQA YEEISKEHLAVYKIQMCKSVKAPGICIDVD NEDLFPIADKNSPDDLSKNERIEYNTQSN
```

```
            481              510 511              540 541              570 571              600
Original_Seq42   YIENDFPINELILDTDLISKIELPSENTES LTDPNVDVPVYEKQPAIKKIFTDENTIFQY LYSQTFPLDIRDISLTSSFDDALLFSNKVY SPFSMDYIKTANKVVEAGLFAGWVKQIVND
Substitute_Seq42 YIENDFPINELILDTDLISKIELPSENTES LTDPNVDVPVYEKQPAIKKIFTDENTIFQY LYSQTFPLDIRDISLTSSFDDALLFSNKVY SPFSMDYIKTANKVVEAGLFAGWVKQIVND
Amended_Seq42    YIENDFPINELILDTDLISKIELPSENTES LTDPNVDVPVYEKQPAIKKIFTDENTIFQY LYSQTFPLDIRDISLTSSFDDALLFSNKVY SPFSMDYIKTANKVVEAGLFAGWVKQIVND
Whelan_M81186    YIENDFPINELILDTDLISKIELPSENTES LTDPNVDVPVYEKQPAIKKIFTDENTIFQY LYSQTFPLDIRDISLTSSFDDALLFSNKVY SPFSMDYIKTANKVVEAGLFAGWVKQIVND
```

```
            601              630 631              660 661              690 691              720
Original_Seq42   FVIEANKSNTMDKIADISLIVPYIGLALNV GNETAKGNFENAPEIAGASILLEFIPELLI PVVGAFLLESYIDNKNKIIKTIDNALTKRN EKWSDMYGLIVAQWLSTVNTQFYTIKEGMY
Substitute_Seq42 FVIEANKSNTMDKIADISLIVPYIGLALNV GNETAKGNFENAPEIAGASILLEFIPELLI PVVGAFLLESYIDNKNKIIKTIDNALTKRN EKWSDMYGLIVAQWLSTVNTQFYTIKEGMY
Amended_Seq42    FVIEANKSNTMDKIADISLIVPYIGLALNV GNETAKGNFENAPEIAGASILLEFIPELLI PVVGAFLLESYIDNKNKIIKTIDNALTKRN EKWSDMYGLIVAQWLSTVNTQFYTIKEGMY
Whelan_M81186    FVIEANKSNTMDKIADISLIVPYIGLALNV GNETAKGNFENAPEIAGASILLEFIPELLI PVVGAFLLESYIDNKNKIIKTIDNALTKRN EKWSDMYGLIVAQWLSTVNTQFYTIKEGMY
```

```
            721              750 751              780 781              810 811              840
Original_Seq42   KALNYQAQALEEIIKYRYNIYSEKEKSNIN IDFNDINSKLNEGINQAIDNINNFINGCSV SYLMKKMIPLAVEKLLDPDNTLKKNLLNYI DENKLYLIGSAEYEKSKVNKYLKTIMPFDL
Substitute_Seq42 KALNYQAQALEEIIKYRYNIYSEKEKSNIN IDFNDINSKLNEGINQAIDNINNFINGCSV SYLMKKMIPLAVEKLLDPDNTLKKNLLNYI DENKLYLIGSAEYEKSKVNKYLKTIMPFDL
Amended_Seq42    KALNYQAQALEEIIKYRYNIYSEKEKSNIN IDFNDINSKLNEGINQAIDNINNFINGCSV SYLMKKMIPLAVEKLLDPDNTLKKNLLNYI DENKLYLIGSAEYEKSKVNKYLKTIMPFDL
Whelan_M81186    KALNYQAQALEEIIKYRYNIYSEKEKSNIN IDFNDINSKLNEGINQAIDNINNFINGCSV SYLMKKMIPLAVEKLLDPDNTLKKNLLNYI DENKLYLIGSAEYEKSKVNKYLKTIMPFDL
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            841              870 871              900 901              930 931              960
Original_Seq42   SIYTNDTILIEMFNKYNSEILNNIILNLRY KDNNLIDLSGYGAKVEVYDGVELNDKNQFK LTSSANSKIR#TQNQNIIFNSVFLDFSVSF WIRIPKYKNDGIQNYIHNEYTIINCMKNNS
Substitute_Seq42 SIYTNDTILIEMFNKYNSEILNNIILNLRY KDNNLIDLSGYGAKVEVYDGVELNDKNQFK LTSSANSKIR#TQNQNIIFNSVFLDFSVSF WIRIPKYKNDGIQNYIHNEYTIINCMKNNS
Amended_Seq42    SIYTNDTILIEMFNKYNSEILNNIILNLRY KDNNLIDLSGYGAKVEVYDGVELNDKNQFK LTSSANSKIR#TQNQNIIFNSVFLDFSVSF WIRIPKYKNDGIQNYIHNEYTIINCMKNNS
Whelan_M81186    SIYTNDTILIEMFNKYNSEILNNIILNLRY KDNNLIDLSGYGAKVEVYDGVELNDKNQFK LTSSANSKIR#TQNQNIIFNSVFLDFSVSF WIRIPKYKNDGIQNYIHNEYTIINCMKNNS
```

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            961              990 991             1020 1021            1050 1051            1080
Original_Seq42   GWKISIRG#RIIWTLIDINGKTKSVFPEYN IREDISEYINRWPFVTITNNLNNAKIYING KLESNTDIKDIREVIANGEIIFKLDGDIDR TQFIWMKYFSIFNTELSQSNIEERYKIQSY
Substitute_Seq42 GWKISIRG#RIIWTLIDINGKTKSVFPEYN IREDISEYINRWPFVTITNNLNNAKIYING KLESNTDIKDIREVIANGEIIFKLDGDIDR TQFIWMKYFSIFNTELSQSNIEERYKIQSY
Amended_Seq42    GWKISIRG#RIIWTLIDINGKTKSVFPEYN IREDISEYINRWPFVTITNNLNNAKIYING KLESNTDIKDIREVIANGEIIFKLDGDIDR TQFIWMKYFSIFNTELSQSNIEERYKIQSY
Whelan_M81186    GWKISIRG#RIIWTLIDINGKTKSVFPEYN IREDISEYINRWPFVTITNNLNNAKIYING KLESNTDIKDIREVIANGEIIFKLDGDIDR TQFIWMKYFSIFNTELSQSNIEERYKIQSY
```

```
            1081            1110 1111            1140 1141            1170 1171            1200
Original_Seq42   SEYLKDFWGNPLMYNKEYYMFNAGNKNSY# IKLKKDSPVGEILTRSKYNQNSKYINYRDL YIGEKFIIRRKSNSQSINDDIVRKEDYIYL DFFNLNQEWRVYTYKYFKKEEE#LFLAPIS
Substitute_Seq42 SEYLKDFWGNPLMYNKEYYMFNAGNKNSY# IKLKKDSPVGEILTRSKYNQNSKYINYRDL YIGEKFIIRRKSNSQSINDDIVRKEDYIYL DFFNLNQEWRVYTYKYFKKEEE#LFLAPIS
Amended_Seq42    SEYLKDFWGNPLMYNKEYYMFNAGNKNSY# IKLKKDSPVGEILTRSKYNQNSKYINYRDL YIGEKFIIRRKSNSQSINDDIVRKEDYIYL DFFNLNQEWRVYTYKYFKKEEE#LFLAPIS
Whelan_M81186    SEYLKDFWGNPLMYNKEYYMFNAGNKNSY# IKLKKDSPVGEILTRSKYNQNSKYINYRDL YIGEKFIIRRKSNSQSINDDIVRKEDYIYL DFFNLNQEWRVYTYKYFKKEEE#LFLAPIS
```

```
            1201            1230 1231            1260 1261            1290 1291 1292
Original_Seq42   DSDEFYNTIQIKEYDEQPTYSCQLLFKKDE ESTDEIGLIGIHRPYESGIVPEE#KD#PCI S#NYL#EVKRKPYNLKLGCNWQPIPKDEGW TE
Substitute_Seq42 DSDEFYNTIQIKEYDEQPTYSCQLLFKKDE ESTDEIGLIGIHRPYESGIVPEE#KD#PCI S#NYL#EVKRKPYNLKLGCNWQPIPKDEGW TE
Amended_Seq42    DSDEFYNTIQIKEYDEQPTYSCQLLFKKDE ESTDEIGLIGIHRPYESGIVPEE#KD#PCI S#WYL#EVKRKPYNLKLGCNWQPIPKDEGW TE
Whelan_M81186    DSDEFYNTIQIKEYDEQPTYSCQLLFKKDE ESTDEIGLIGIHRPYESGIVPEE#KD#PCI S#WYL#EVKRKPYNLKLGCNWQPIPKDEGW TE
```